

ATGGACAAADACACATGTCCACCTTGTCCAGCTCCGGAACCTCCGGACCGTCA
 1 -----+-----+-----+-----+-----+ 60
 TACCTGTTTTGAGTGTGTACAGGTGGAACAGGTTCGAGGCCTTGAGGACCCCCCTGGCAGT
 a M D K T H T C P P C P A P E L L G G P S
 GTCTTCCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC
 61 -----+-----+-----+-----+-----+ 120
 CAGAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAG
 a V F L F P P K P K D T L M I S R T P E V
 ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTG
 121 -----+-----+-----+-----+-----+ 180
 TGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCAC
 a T C V V V D V S H E D P E V K F N W Y V
 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAGC
 181 -----+-----+-----+-----+-----+ 240
 CTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGC
 a D G V E V H N A K T K P R E E Q Y N S T
 TACCGTGTGGTCAAGCTCCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
 241 -----+-----+-----+-----+-----+ 300
 ATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTTCTCATG
 a Y R V V S V L T V L H Q D W L N G K E Y
 AAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCC
 301 -----+-----+-----+-----+-----+ 360
 TTCACGTTCCAGAGGTGTGTTTCGGGAGGGTTCGGGGTAGCTCTTTGGTAGAGGTTTCGG
 a K C K V S N K A L P A P I E K T I S K A
 AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC
 361 -----+-----+-----+-----+-----+ 420
 TTTCCCGTTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGTAGGGCCCTACTCGACTGG
 a K G Q P R E P Q V Y T L P P S R D E L T
 AAGAACCAGGTGAGCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG
 421 -----+-----+-----+-----+-----+ 480
 TTCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTAGCGGCAC
 a K N Q V S L T C L V K G F Y P S D I A V
 GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGTGGAC
 481 -----+-----+-----+-----+-----+ 540
 CTCACCCTCTCGTTACCGTTCGGCCTCTTGTGATGTTCTGGTGGGAGGGCAGACCTG
 a E W E S N G Q P E N N Y K T T P P V L D
 TCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
 541 -----+-----+-----+-----+-----+ 600
 AGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTC
 a S D G S F F L Y S K L T V D K S R W Q Q
 GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG
 601 -----+-----+-----+-----+-----+ 660
 CCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGTGTCGCTCTTC
 a G N V F S C S V M H E A L H N H Y T Q K
 AGCCTCTCCCTGTCTCCGGGTAAA
 661 -----+-----+-----+-----+ 684
 TCGGAGAGGGACAGAGGCCCATTT
 a S L S L S P G K

FIGURE 1

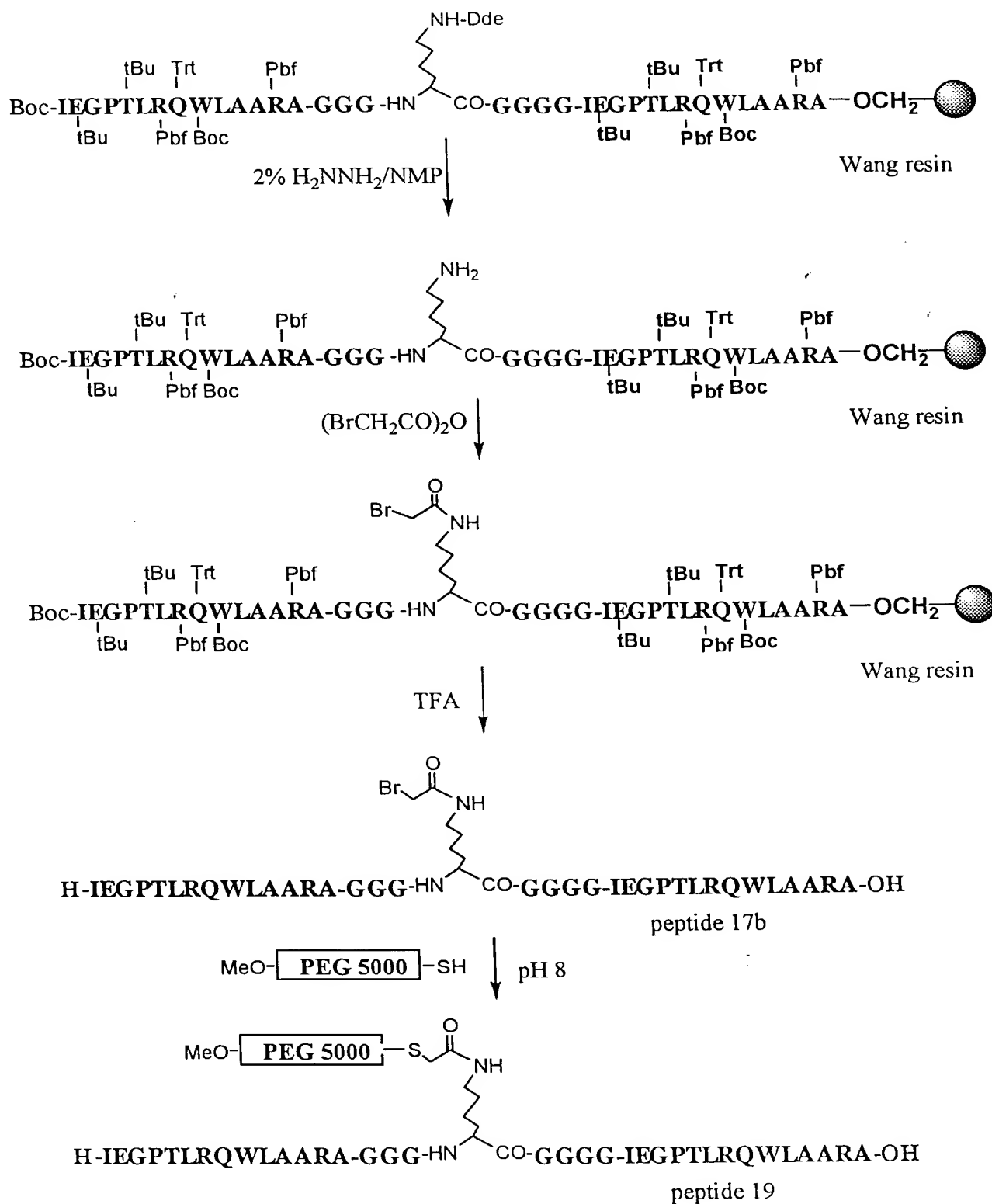


FIGURE 2

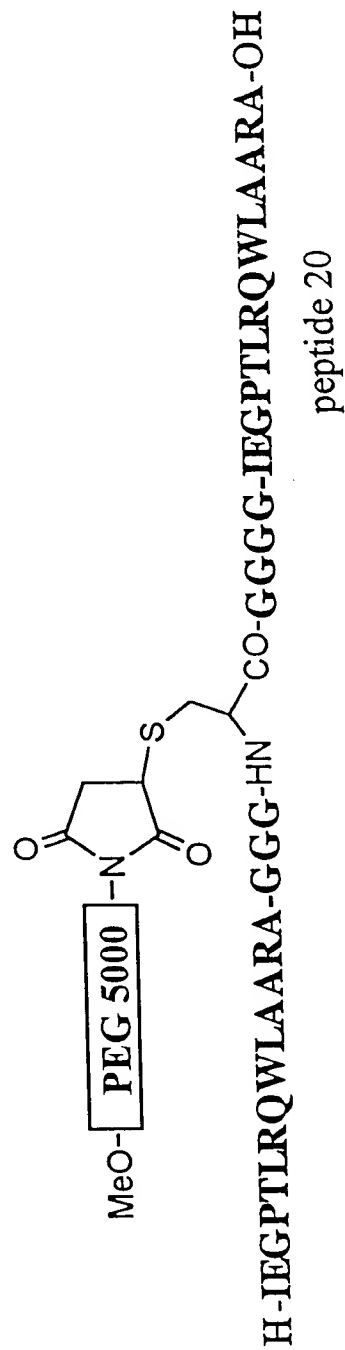
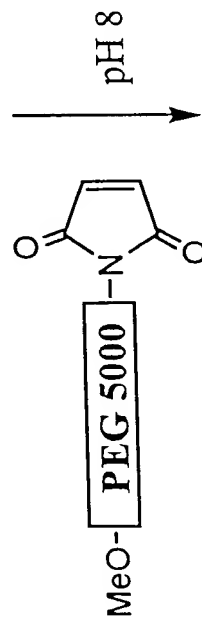
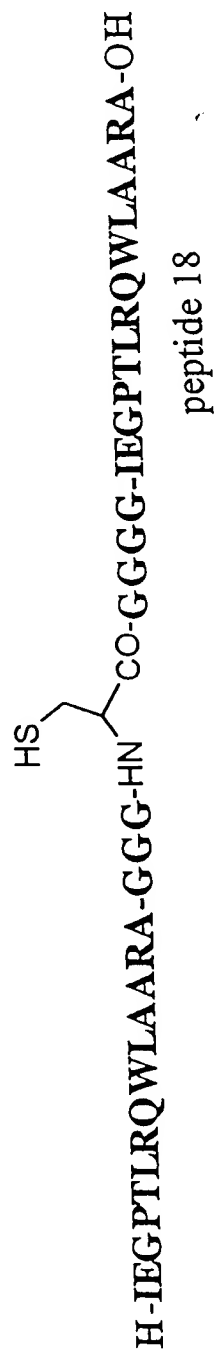
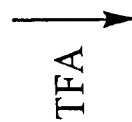
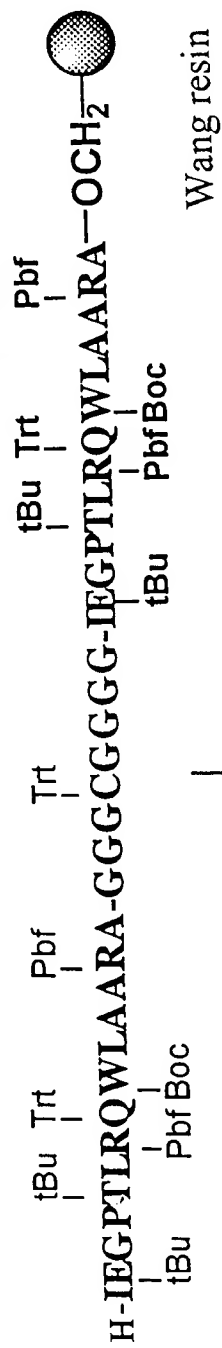


FIGURE 3

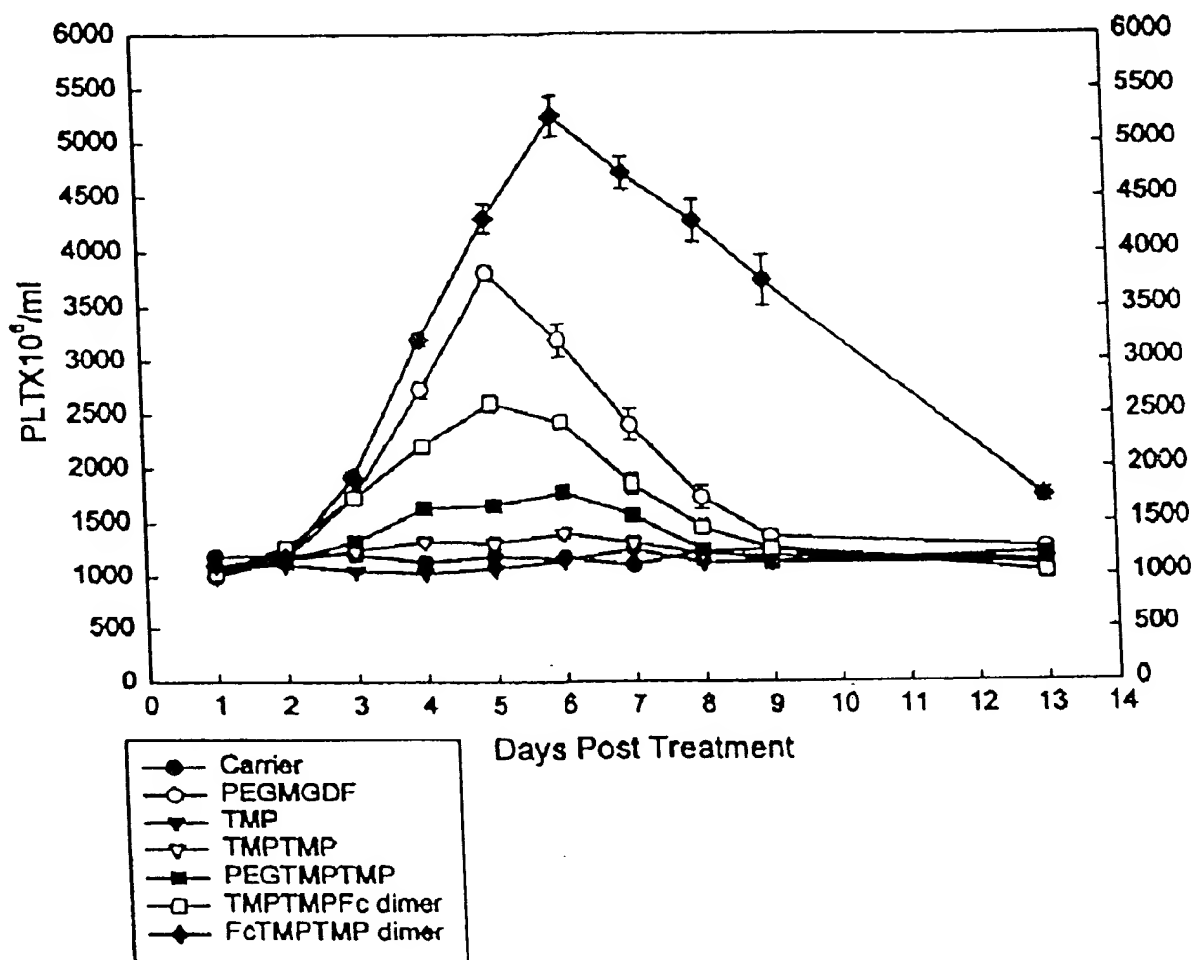


FIGURE 4

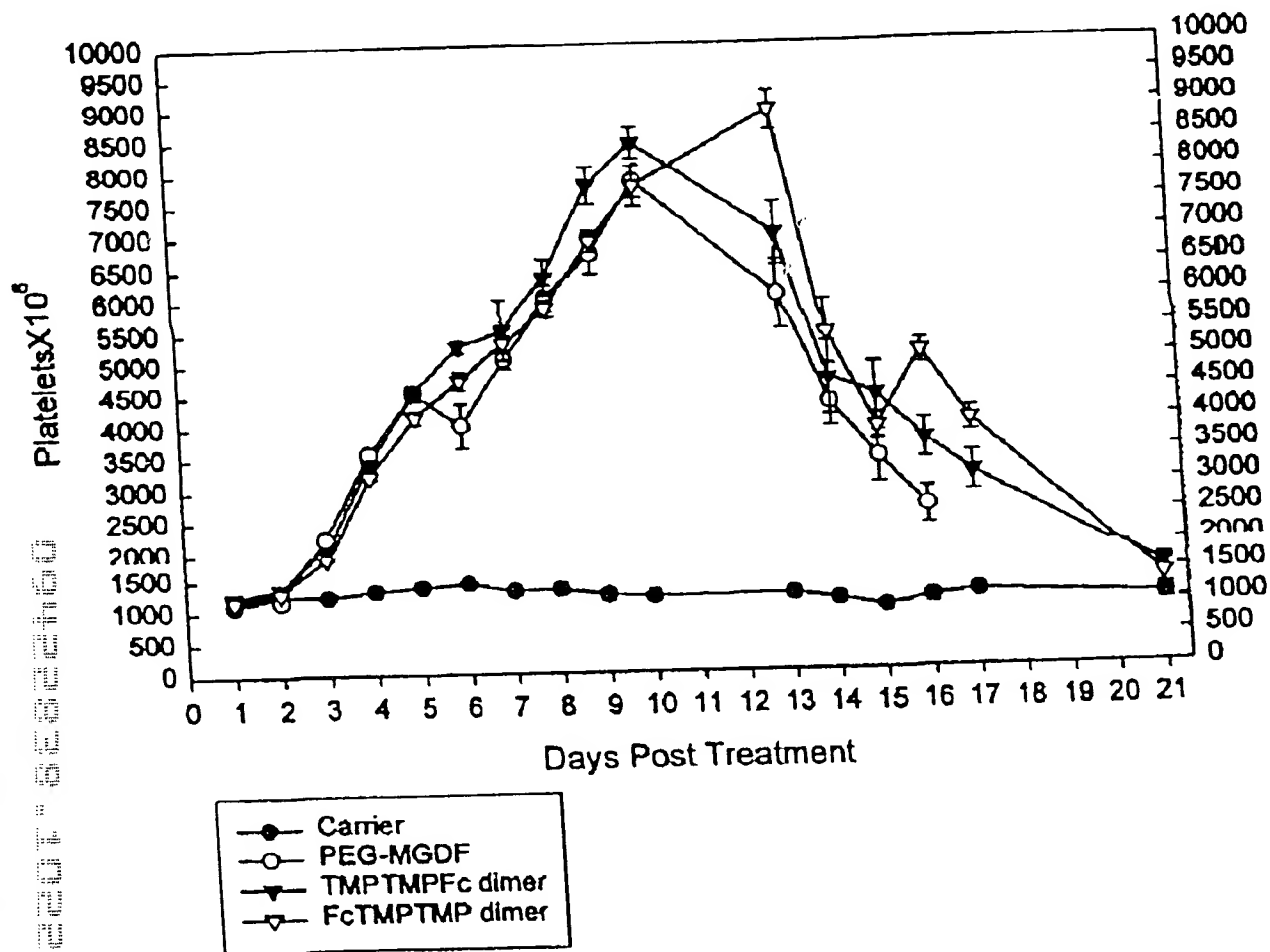


FIGURE 5

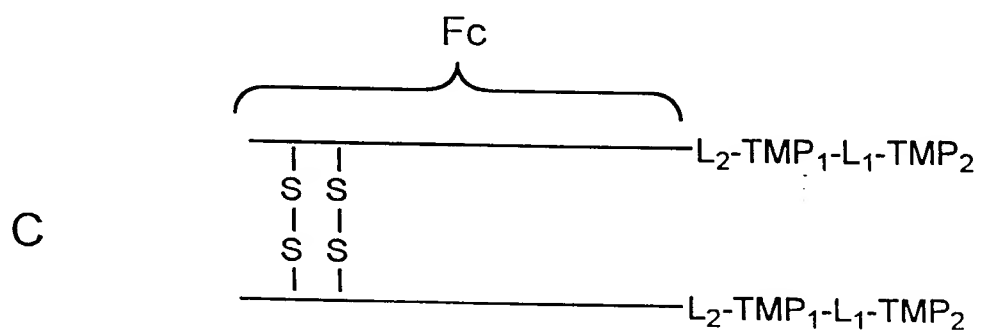
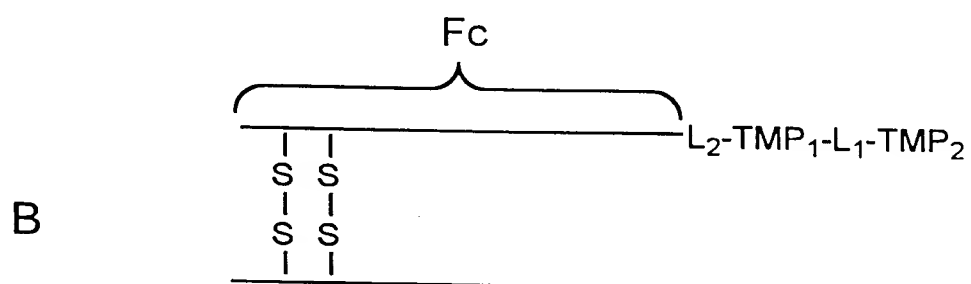
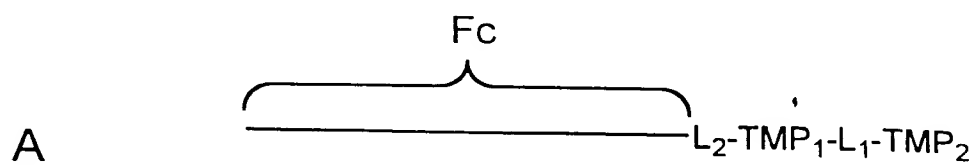


FIGURE 6